



1

SEQUENCE LISTING  
*#140*

*100230*  
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Nakagawa, Hitoshi  
Director General of National Institute of Agrobiological Resources, Ministry of Agriculture, Forestry and Fisheries

<120> Method for Shortening Internode of Inflorescence by Introducing Gene for Petunia Transcription Factor PetSPL2

<130> 085761-000400US

<140> US 09/156,580  
<141> 1998-09-18

<150> JP 10-224852  
<151> 1998-08-07

<160> 18

<170> PatentIn Ver. 2.0

<210> 1  
<211> 997  
<212> DNA  
<213> Petunia hybrida var. Mitchell

<220>  
<221> CDS  
<222> (190)..(810)  
<223> PetSPL2 transcription factor

<400> 1  
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tgcagtaaca ctcctattta accctcacaa aaaaattacc agagggcagc aaaaaatgct 120  
tgaacataat tattatactt actattaagc tagatttcct cttgatcttg cttagtttga 180  
ctggagaaa atg gca ggc atg gat aga aac agt ttc aac agt aag tac ttc 231  
Met Ala Gly Met Asp Arg Asn Ser Phe Asn Ser Lys Tyr Phe  
1 5 10

aaa aac aaa agc atc atg gca aga cag atg gag tac ttg aat aac aac 279  
Lys Asn Lys Ser Ile Met Ala Arg Gln Met Glu Tyr Leu Asn Asn Asn  
15 20 25 30

aat ggc gac aat aac aac aat aat gtt aca agc tca tta cga gat 327  
Asn Gly Asp Asn Asn Asn Asn Asn Val Thr Ser Ser Leu Arg Asp  
35 40 45

aat tat gga aat gaa gat cat tta ctt ggt gga cta ttc tct tgg cct 375  
Asn Tyr Gly Asn Glu Asp His Leu Leu Gly Gly Leu Phe Ser Trp Pro  
50 55 60

cca aga tct tat aca tgt agc ttt tgt aaa agg gaa ttt aga tct gct 423  
Pro Arg Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala  
65 70 75

*23*

caa gct ctt ggt gga cac atg aat gtt cat aga aga gat aga gcc att 471  
 Gln Ala Leu Gly Gly His Met Asn Val His Arg Arg Asp Arg Ala Ile  
   80                       85                       90  
  
 ttg aga caa tca cca cct aga gat att aat agg tat tct ctt cta aac 519  
 Leu Arg Gln Ser Pro Pro Arg Asp Ile Asn Arg Tyr Ser Leu Leu Asn  
   95                       100                       105                       110  
  
 ctt aat ctt gaa cca aac cct aac ttt tac cct agt cat aac cct agt 567  
 Leu Asn Leu Glu Pro Asn Pro Phe Tyr Pro Ser His Asn Pro Ser  
   115                       120                       125  
  
 ttt tca aga aaa ttc cca cct ttt gaa atg agg aaa tta gga aaa gga 615  
 Phe Ser Arg Lys Phe Pro Pro Phe Glu Met Arg Lys Leu Gly Lys Gly  
   130                       135                       140  
  
 gtt gtt cca aac aat cac ttg aaa agt gcc aga ggg cgt ttt gga gtt 663  
 Val Val Pro Asn Asn His Leu Lys Ser Ala Arg Gly Arg Phe Gly Val  
   145                       150                       155  
  
 gag aaa att gac tct ttc atg caa gaa aaa gaa tgt act act aca gtg 711  
 Glu Lys Ile Asp Ser Phe Met Gln Glu Lys Glu Cys Thr Thr Thr Val  
   160                       165                       170  
  
 atc aag aag tcc gag ttt cta aga ttg gac ttg gga att ggg ttg atc 759  
 Ile Lys Lys Ser Glu Phe Leu Arg Leu Asp Leu Gly Ile Gly Leu Ile  
   175                       180                       185                       190  
  
 agt gaa tca aag gaa gat tta gat ctt gaa ctt cga ctg gga tcc act 807  
 Ser Glu Ser Lys Glu Asp Leu Asp Leu Glu Leu Arg Leu Gly Ser Thr  
   195                       200                       205  
  
 taactatac taattttac ggcattaagg tttgtaaatt gagtcgacag cttagtcaaa 867  
 actacttag cacttaata tggcttcttg tgctatattt atttatttta catggctgta 927  
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<210> 2  
 <211> 206  
 <212> PRT  
 <213> Petunia sp.

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 Lys Ser Ile Met Ala Arg Gln Met Glu Tyr Leu Asn Asn Asn Gly  
   20                       25                       30  
  
 Asp Asn Asn Asn Asn Asn Val Thr Ser Ser Leu Arg Asp Asn Tyr  
   35                       40                       45  
  
 Gly Asn Glu Asp His Leu Leu Gly Gly Leu Phe Ser Trp Pro Pro Arg  
   50                       55                       60  
  
 Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala  
   65                       70                       75                       80

24

Leu Gly Gly His Met Asn Val His Arg Arg Asp Arg Ala Ile Leu Arg  
 85 90 95

Gln Ser Pro Pro Arg Asp Ile Asn Arg Tyr Ser Leu Leu Asn Leu Asn  
 100 105 110

Leu Glu Pro Asn Pro Asn Phe Tyr Pro Ser His Asn Pro Ser Phe Ser  
 115 120 125

Arg Lys Phe Pro Pro Phe Glu Met Arg Lys Leu Gly Lys Gly Val Val  
 130 135 140

Pro Asn Asn His Leu Lys Ser Ala Arg Gly Arg Phe Gly Val Glu Lys  
 145 150 155 160

Ile Asp Ser Phe Met Gln Glu Lys Glu Cys Thr Thr Thr Val Ile Lys  
 165 170 175

Lys Ser Glu Phe Leu Arg Leu Asp Leu Gly Ile Gly Leu Ile Ser Glu  
 180 185 190

Ser Lys Glu Asp Leu Asp Leu Glu Leu Arg Leu Gly Ser Thr  
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<210> 3

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:degenerate  
 primer 1

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<221> modified\_base

<222> (6)

<223> i

<220>

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<222> (12)

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<221> modified\_base

<222> (15)

<223> i

<400> 3

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<210> 4
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
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<220>
<221> modified_base
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<400> 4
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18

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<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
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      primer 3

<220>
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<220>
<221> modified_base
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<400> 5
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17

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<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence
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26

&lt;220&gt;

<223> Description of Artificial Sequence:amino acids  
present in both SUPERMAN gene of Arabidopsis  
thaliana and GmN479 gene of soy bean root nodules

&lt;400&gt; 6

Gln Ala Leu Gly Gly His  
1 5

&lt;210&gt; 7

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:amino acids  
present in both SUPERMAN gene of Arabidopsis  
thaliana and GmN479 gene of soy bean root nodules

&lt;400&gt; 7

Leu Gly Gly His Met Asn  
1 5

&lt;210&gt; 8

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:amino acids  
present in both SUPERMAN gene of Arabidopsis  
thaliana and GmN479 gene of soy bean root nodules

&lt;400&gt; 8

Asp Leu Glu Leu Arg Leu  
1 5

&lt;210&gt; 9

&lt;211&gt; 43

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:SUPERMAN zinc  
finger motif

&lt;400&gt; 9

Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala  
1 5 10 15

Leu Gly Gly His Met Asn Val His Arg Arg Asp Arg Ala Arg Leu Arg  
20 25 30

Leu Gln Gln Ser Pro Ser Ser Ser Thr Pro  
35 40

27

<210> 10  
<211> 42  
<212> PRT  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: PetSPL1 zinc finger motif

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Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala  
1 5 10 15  
  
Leu Gly Gly His Met Asn Val His Arg Arg Asp Arg Ala Arg Leu Arg  
20 25 30  
  
Leu Gln Ser Pro Pro Arg Glu Asn Gly Thr  
35 40

<210> 11  
<211> 41  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PetSPL2 zinc finger motif

<400> 11  
Ser Tyr Thr Cys Ser Phe Cys Lys Arg Glu Phe Arg Ser Ala Gln Ala  
1 5 10 15  
  
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20 25 30  
  
Gln Ser Pro Pro Arg Asp Ile Asn Arg  
35 40

<210> 12  
<211> 43  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: PetSPL3 zinc finger motif

<400> 12  
Ser Tyr Glu Cys Asn Phe Cys Lys Arg Gly Phe Ser Asn Ala Gln Ala  
1 5 10 15  
  
Leu Gly Gly His Met Asn Ile His Arg Lys Asp Lys Ala Lys Leu Lys  
20 25 30  
  
Lys Gln Lys Gln His Gln Arg Gln Gln Lys Pro  
35 40



<210> 13  
<211> 43  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence:PetSPL4 zinc finger motif

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Phe Tyr Arg Cys Ser Phe Cys Lys Arg Gly Phe Ser Asn Ala Gln Ala  
1 5 10 15  
Leu Gly Gly His Met Asn Ile His Arg Lys Asp Arg Ala Lys Leu Arg  
20 25 30  
Glu Ile Ser Thr Asp Asn Leu Asn Ile Asp Gln  
35 40

<210> 14  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:SUPERMAN  
C-terminal hydrophobic region

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Ile Asn Glu Ser Glu Gln Asp Leu Asp Leu Glu Leu Arg Leu Gly Phe  
20 25 30

Ala

<210> 15  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
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C-terminal hydrophobic region

<400> 15  
Leu Met Lys Arg Ser Glu Phe Leu Arg Leu Glu Leu Gly Ile Gly Met  
1 5 10 15  
Ile Asn Glu Ser Lys Glu Asp Leu Asp Leu Glu Leu Arg Leu Gly Tyr  
20 25 30

Thr

29

<210> 16  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Pet SPL2  
C-terminal hydrophobic region

<400> 16  
Val Ile Lys Lys Ser Glu Phe Leu Arg Leu Asp Leu Gly Ile Gly Leu  
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20 25 30

Thr

<210> 17  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PetSPL3  
C-terminal hydrophobic region

<400> 17  
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Thr Thr Pro Phe Tyr Ala Glu Leu Asp Leu Glu Leu Arg Leu Gly His  
20 25 30

Glu

<210> 18  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PetSPL4  
C-terminal hydrophobic region

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Met Gln Gln Asp Asp Ser Lys Leu Asp Leu Glu Leu Arg Leu Gly Pro  
20 25 30

Asp

30